



Corrected sequence listing 11-07
SEQUENCE LISTING

<110> Consortium fuer elektrochemische Industrie GmbH

<120> Feedback-resistant Homoserine-Transsuccinylases

<130> CO-P#####

<140> 10530843

<141> 2007-11-14

<160> 12

<170> PatentIn Ver. 2.0

<210> 1

<211> 930

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)..(930)

<300>

<301> Blattner, F. R.

<302> The complete genome sequence of Escherichia coli K-12.

<303> Science

<304> 277

<305> 5331

<306> 1453-1474

<307> 1997

<400> 1

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| atg | ccg | att | cgt | gtg | ccg | gac | gag | cta | ccc | gcc | gtc | aat | ttc | ttg | cgt | 48 |
| Met | Pro | Ile | Arg | Val | Pro | Asp | Glu | Leu | Pro | Ala | Val | Asn | Phe | Leu | Arg | |
| 1 | | | | 5 | | | | 10 | | | | | | 15 | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| gaa | gaa | aac | gtc | ttt | gtg | atg | aca | act | tct | cgt | gcg | tct | ggt | cag | gaa | 96 |
| Glu | Glu | Asn | Val | Phe | Val | Met | Thr | Thr | Ser | Arg | Ala | Ser | Gly | Gln | Glu | |
| | | 20 | | | | | | 25 | | | | | 30 | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| att | cgt | cca | ctt | aag | gtt | ctg | atc | ctt | aac | ctg | atg | ccg | aag | aag | att | 144 |
| Ile | Arg | Pro | Leu | Lys | Val | Leu | Ile | Leu | Asn | Leu | Met | Pro | Lys | Lys | Ile | |
| | | 35 | | | | 40 | | | | | | 45 | | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| gaa | act | gaa | aat | cag | ttt | ctg | cgc | ctg | ctt | tca | aac | tca | cct | ttg | cag | 192 |
| Glu | Thr | Glu | Asn | Gln | Phe | Leu | Arg | Leu | Leu | Ser | Asn | Ser | Pro | Leu | Gln | |
| | 50 | | | | | 55 | | | | | 60 | | | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| gtc | gat | att | cag | ctg | ttg | cgc | atc | gat | tcc | cgt | gaa | tcg | cgc | aac | acg | 240 |
| Val | Asp | Ile | Gln | Leu | Leu | Arg | Ile | Asp | Ser | Arg | Glu | Ser | Arg | Asn | Thr | |
| 65 | | | | 70 | | | | 75 | | | | | | | 80 | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| ccc | gca | gag | cat | ctg | aac | aac | ttc | tac | tgt | aac | ttt | gaa | gat | att | cag | 288 |
| Pro | Ala | Glu | His | Leu | Asn | Asn | Phe | Tyr | Cys | Asn | Phe | Glu | Asp | Ile | Gln | |
| | | | | 85 | | | | 90 | | | | | | 95 | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| gat | cag | aac | ttt | gac | ggt | ttg | att | gta | act | ggt | gcg | ccg | ctg | ggc | ctg | 336 |
| Asp | Gln | Asn | Phe | Asp | Gly | Leu | Ile | Val | Thr | Gly | Ala | Pro | Leu | Gly | Leu | |
| | | 100 | | | | | | 105 | | | | | 110 | | | |

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| | |
|---|-----|
| gtg gag ttt aat gat gtc gct tac tgg ccg cag atc aaa cag gtg ctg | 384 |
| Val Glu Phe Asn Asp Val Ala Tyr Trp Pro Gln Ile Lys Gln Val Leu | |
| 115 120 125 | |
| gag tgg tcg aaa gat cac gtc acc tcg acg ctg ttt gtc tgc tgg gcg | 432 |
| Glu Trp Ser Lys Asp His Val Thr Ser Thr Leu Phe Val Cys Trp Ala | |
| 130 135 140 | |
| gta cag gcc gcg ctc aat atc ctc tac ggc att cct aag caa act cgc | 480 |
| Val Gln Ala Ala Leu Asn Ile Leu Tyr Gly Ile Pro Lys Gln Thr Arg | |
| 145 150 155 160 | |
| acc gaa aaa ctc tct ggc gtt tac gag cat cat att ctc cat cct cat | 528 |
| Thr Glu Lys Leu Ser Gly Val Tyr Glu His His Ile Leu His Pro His | |
| 165 170 175 | |
| gcg ctt ctg acg cgt ggc ttt gat gat tca ttc ctg gca ccg cat tcg | 576 |
| Ala Leu Leu Thr Arg Gly Phe Asp Asp Ser Phe Leu Ala Pro His Ser | |
| 180 185 190 | |
| cgc tat gct gac ttt ccg gca gcg ttg att cgt gat tac acc gat ctg | 624 |
| Arg Tyr Ala Asp Phe Pro Ala Ala Leu Ile Arg Asp Tyr Thr Asp Leu | |
| 195 200 205 | |
| gaa att ctg gca gag acg gaa gaa ggg gat gca tat ctg ttt gcc agt | 672 |
| Glu Ile Leu Ala Glu Thr Glu Glu Gly Asp Ala Tyr Leu Phe Ala Ser | |
| 210 215 220 | |
| aaa gat aag cgc att gcc ttt gtg acg ggc cat ccc gaa tat gat gcg | 720 |
| Lys Asp Lys Arg Ile Ala Phe Val Thr Gly His Pro Glu Tyr Asp Ala | |
| 225 230 235 240 | |
| caa acg ctg gcg cag gaa ttt ttc cgc gat gtg gaa gcc gga cta gac | 768 |
| Gln Thr Leu Ala Gln Glu Phe Phe Arg Asp Val Glu Ala Gly Leu Asp | |
| 245 250 255 | |
| ccg gat gta ccg tat aac tat ttc ccg cac aat gat ccg caa aat aca | 816 |
| Pro Asp Val Pro Tyr Asn Tyr Phe Pro His Asn Asp Pro Gln Asn Thr | |
| 260 265 270 | |
| ccg cga gcg agc tgg cgt agt cac ggt aat tta ctg ttt acc aac tgg | 864 |
| Pro Arg Ala Ser Trp Arg Ser His Gly Asn Leu Leu Phe Thr Asn Trp | |
| 275 280 285 | |
| ctc aac tat tac gtc tac cag atc acg cca tac gat cta cgg cac atg | 912 |
| Leu Asn Tyr Tyr Val Tyr Gln Ile Thr Pro Tyr Asp Leu Arg His Met | |
| 290 295 300 | |
| aat cca acg ctg gat taa | 930 |
| Asn Pro Thr Leu Asp | |
| 305 | |

<210> 2

<211> 309

<212> PRT

<213> Escherichia coli

<400> 2

Met Pro Ile Arg Val Pro Asp Glu Leu Pro Ala Val Asn Phe Leu Arg

1

5

10

15

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Glu Glu Asn Val Phe Val Met Thr Thr Ser Arg Ala Ser Gly Gln Glu
20 25 30
Ile Arg Pro Leu Lys Val Leu Ile Leu Asn Leu Met Pro Lys Lys Ile
35 40 45
Glu Thr Glu Asn Gln Phe Leu Arg Leu Leu Ser Asn Ser Pro Leu Gln
50 55 60
Val Asp Ile Gln Leu Leu Arg Ile Asp Ser Arg Glu Ser Arg Asn Thr
65 70 75 80
Pro Ala Glu His Leu Asn Asn Phe Tyr Cys Asn Phe Glu Asp Ile Gln
85 90 95
Asp Gln Asn Phe Asp Gly Leu Ile Val Thr Gly Ala Pro Leu Gly Leu
100 105 110
Val Glu Phe Asn Asp Val Ala Tyr Trp Pro Gln Ile Lys Gln Val Leu
115 120 125
Glu Trp Ser Lys Asp His Val Thr Ser Thr Leu Phe Val Cys Trp Ala
130 135 140
Val Gln Ala Ala Leu Asn Ile Leu Tyr Gly Ile Pro Lys Gln Thr Arg
145 150 155 160
Thr Glu Lys Leu Ser Gly Val Tyr Glu His His Ile Leu His Pro His
165 170 175
Ala Leu Leu Thr Arg Gly Phe Asp Asp Ser Phe Leu Ala Pro His Ser
180 185 190
Arg Tyr Ala Asp Phe Pro Ala Ala Leu Ile Arg Asp Tyr Thr Asp Leu
195 200 205
Glu Ile Leu Ala Glu Thr Glu Glu Gly Asp Ala Tyr Leu Phe Ala Ser
210 215 220
Lys Asp Lys Arg Ile Ala Phe Val Thr Gly His Pro Glu Tyr Asp Ala
225 230 235 240
Gln Thr Leu Ala Gln Glu Phe Phe Arg Asp Val Glu Ala Gly Leu Asp
245 250 255
Pro Asp Val Pro Tyr Asn Tyr Phe Pro His Asn Asp Pro Gln Asn Thr
260 265 270
Pro Arg Ala Ser Trp Arg Ser His Gly Asn Leu Leu Phe Thr Asn Trp
275 280 285
Leu Asn Tyr Tyr Val Tyr Gln Ile Thr Pro Tyr Asp Leu Arg His Met
290 295 300
Asn Pro Thr Leu Asp
305

<210> 3

<211> 30

<212> DNA

<213> Artificial Sequence

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<220>
 <223> Description of Artificial Sequence:
 Oligonucleotide metAfw

<400> 3
 gatcccatgg ctccttttag tcattcttat 30

<210> 4
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Oligonucleotide
 metArev

<400> 4
 gatcgagctc agtactatta atccagcggt ggattc 36

<210> 5
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Oligonucleotide
 GAPDHfw

<400> 5
 gtcgacgcgt gaggcgagtc agtcgcgtaa tgc 33

<210> 6
 <211> 42
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Oligonucleotide
 GAPDHrevII

<400> 6
 gaccttaatt aagatctcat atgttccacc agctatttgt ta 42

<210> 7
 <211> 37
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Oligonucleotide
 metAfw2

<400> 7
 catggctcct tttagtcatt cttatattct aacgtag 37

<210> 8
 <211> 47

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<212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: Oligonucleotide
 metArev2
 <400> 8
 acgcgtatgc atccagagct cagtactatt aatccagcgt tggattc 47
 <210> 9
 <211> 25
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: Oligonucleotide
 metAmutfw1; n=1:1:1:1 mixture of A,T,C and G.
 <400> 9
 nnncagatca cgccatacga tctac 25
 <210> 10
 <211> 23
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: Oligonucleotide
 metAmutrev1
 <400> 10
 gacgtaatag ttgagccagt tgg 23
 <210> 11
 <211> 24
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: Oligonucleotide
 metAmutfw2; N is a 1:1:1:1: mixture of A, T, C and G
 <400> 11
 nnnggtttga ttgtaactgg tgcg 24
 <210> 12
 <211> 21
 <212> DNA
 <213> Artificial Sequence
 <220>

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<223> Description of Artificial Sequence: Oligonucleotide
metAmutrev2

<400> 12

aaagttctga tcctgaatat c

21